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AMENDMENTS

TO THE SPECIFICATION

On page 6, please amend paragraph [0022] as follows:

FIG. 2C depicts a sequence alignment of the central, hydrophilic region of hCdc5 (SEQ ID No: 7), a putative activating domain of *S. pombe Cdc5* (SEQ ID NO: 3) (SEQ ID NO: 8), and the activating domains of a- and b-Myb (SEQ ID No.: 10 and 9, respectively). Prolines are highlighted in bold. Gaps (-) were introduced to maximize alignment.

On page 7, please amend paragraph [0028] as follows:

Figure 6 comprises panels A H and depicts the results of flow cytometry of 3T15.8.22 cultures synchronized in G0 by growth for 48 hours in media made 0.5% serum with or without tetracycline, released from quiescence by addition of serum to 10%, and analyzed at indicated timepoints. Cells were stained with propidium iodide and Hoechst 33342 to determine viability and DNA content, respectively. The experiment was repeated 5 times, with a representative study shown.

On page 54, please amend paragraph [00202] as follows:

In order to assess the effect of increased hCdc5 expression on cell cycle progression, 3T15.8.22 cells were synchronized in G0 with low serum then released in G1 and measured for DNA content as a function of time (FIG. 6, panels A H). Induction of hCdc5 by removal of tetracycline caused accelerated progression through the cell cycle; cells returned to G1 by 18 hours after release from quiescence in the absence of tetracycline compared with 24 hours in the presence of tetracycline. By contrast, the parent cell line 3T15.8, which expressed the tet repressor-VP16 fusion but not exogenous hCdc5, return to G1 by 24 hours without any tetracycline-dependent effect. This cell cycle acceleration was maintained over time (FIG. 7). Over 72 hours, cells overexpressing hCdc5 exhibited an abbreviated cell cycle length of about 19 hours, while cells in

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which recombinant hCdc5 expression was repressed by tetracycline grew at a slower rate with a cycle length of about 28 hours. The cell cycle length in 3T15.8 cultures was about 26 hours, unaffected by tetracycline, and similar to that seen in 3T15.8.22 cultures in the presence of tetracycline.